

SEQUENCE LISTING

SEQ ID NO: 1 - SARS Coronavirus Urbani S-protein full-length gene sequence (AY278741, 3768 bps)

atgtttattttctattatttctactctactagtgtagtgaccttgaccggtgcaccacttttgatgatgttcaagctcc
taattacactcaacatacttcatctatgaggggggttactatcctgatgaaatttttagatcagacactctttatttaactcag
gattatttcttccattttatttctaattgttacagggttcatactattaatcatacgtttggcaaccctgtcatacctttaaggat
ggtattttttgctgccacagagaaatcaaatgttgccgtggttgggttttgggttctacatgaacaacaagtcacagtc
ggtgattattttaacaatttactaatgttggtatgacgagcatgtaactttgaattgtgtgacaacccttcttctgctgttctaa
acccatgggtacacagacacatactatgatattcgataatgcatttaattgcacttctgagtacatatctgatgccttttcgc
ttgatgtttcagaaaaagtcaggtaattttaaacacttacgagagttgtgtttaaaaataaagatgggttctctatgtttataa
gggctatcaacctatagatgtagttcgtgatctaccttctgggtttaaacactttgaaacctattttaagttgcctcttggtatta
acattacaaatttttagagccattcttacagcctttcacctgctcaagacatttggggcacgtcagctgcagcctattttgtt
ggctatttaaagccaactacatttatgctcaagtatgatgaaatggtacaatcacagatgctgttgattgttctcaaaatcc
acttgcgtgaactcaaatgctctgttaagagctttgagattgacaaaggaatttaccagacctctaatttcagggttgttccct
caggagatgttgtagattccctaataattacaaactgtgtcctttggagaggttttaattgctactaaattcccttctgtcta
tgcatgggagagaaaaaaatttctaattgtgtgctgattactctgtgctctacaactcaacattttttcacctttaagt
ctatggcggtttctgccactaagttgaatgatctttgcttccaatgtctatgcagattctttttagtcaaggagatgatgt
aagacaaatagcgccaggacaaactggtgtattgctgattataattataaattgccagatgattcatgggtgtgtcctt
gcttggaaactaggaacattgatgctacttcaactggtaattataaattataaattataggtatcttagacatggcaagcttag
gccctttgagagagacatactaatgtgcctttctcccctgatggcaaaccttgcacccacctgctcttaattgttattggc
cattaaatgattatggtttttacaccactactggcattggctaccaaccttacagagttgtagtactttctttgaacttttaaat
gcaccggccacggtttgtggacaaaattatccactgaccttattaagaaccagtgtgtcaattttaatttaattggaactca
ctggtactggtgtgttaactccttctcaaagagatttcaaccatttcaacaatttggccgtgatgttctgatttactgattc
cgttcgagatcctaaaacatctgaaatattagacatttcccttgccttttgggggtgtaagtgaattacacctggaaca
aatgcttcatctgaagtgtgtgtcttatcaagatgttaactgcactgatgtttctacagcaattcatgcagatcaactcac
accagcttggcgcatatatttacttgaaacaatgtattccagactcaagcaggctgtcttataggagctgagcatgtcg
acacttctatgagtgcgacattcctattggagctggcatttgtgctagtaccatacagttctttattacgtagtactagcc
aaaaatctatttggcttatactatgtcttttaggtgctgatagttcaattgcttacttctaataacaccattgctatacctactaa
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aacaggatcgcaacacacgtgaagtgttcgctcaagtcaacaatgtacaaaaccccaacttgaatatatttgggtgtg
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ttcaatggacttacagtgttgcaccctctgctcactgatgataatgctgcctacactgctgctctagttagtggtactgc
cactgctggatggacatttgggtgctggcgctgctcttcaaataccttttgcctatgcaaatggcatataggttcaatggcatt
ggagttacccaaaatgttctctatgagaacaaaaacaaatcgccaaccaatttaacaaggcgattagtaaattcaaga
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ttaacaacttagctctaattttgtgcaatttcaagtgtgctaaatgatattcctttcgcgacttgataaagtcgaggcggag
gtacaaattgacagggttaattacaggcagacttcaaagccttcaaacctatgtaacacaacaactaatcagggtgctgta
aatcagggtcttgcctaatttgcgtgctactaaaatgtctgagtgtgttcttggacaatcaaaaagagttgacttttggaa
agggttaccaccttatgtccttcccacaagcagccccgatggtgtgtcttctacatgtcacgtatgtgccatcccag
gagaggaacttaccacagcgccagcaatttgcattgaaggcaaaagcatacttccctcgtgaaggtgttttgtgtttaat
ggcacttcttgggttattacacagaggaacttcttctccacaataattactacagacaataatttgcctcaggaaattgt
gatgtcgttattggcatcattaacaacacagtttatgatcctctgcaacctgagctcgactcattcaagaagagctggac
aagtacttcaaaaatcatacatcaccagatgttgatcttggcgacatttcaggcattaacgccttctgtcgtcaacattcaaa

aagaaattgaccgcctcaatgaggtcgctaaaaatttaaatgaatcactcattgaccttcaagaattgggaaaatatgag
caatatattaaatggccttggatgtttggctcggcttcattgctggactaattgccatcgatggttacaatcttgdttgtt
gcatgactagtgttgacgttgcctcaaggggtgcatgctcttggttcttgctgcaagttgatgaggatgactctgagcc
agtctcaaggggtgtcaaattacattacataa

SEQ ID NO: 2 - Protein sequence for full length S-protein from accession number AAP13441 corresponding to the gene AY278741 (1256aa)

MFIFLLFLTSTSGSDLDRCTTFDDVQAPNYTQHTSSMRGVYYPDEIFRS
DTLYLTQDLFLPFYSNVTGFHTINHTFGNPVIPFKDGIYFAATEKSNVVRG
WVFGSTMNNKSQSVMNNSTNVVIRACNFELCDNPFFAVSKPMGTQTHTM
IFDNAFNCTFEYISDAFSLDVSEKSGNFKHLREFVFKNKDGFLYVYKGYQPI
DVVRDLPSGFNTLKPIFKLPLGINITNFRAILTAFSPAQDWGTSAAA YFVG
YLKPTTFMLKYDENGITITDAVDCSQNPLAELKCSVKSFEDKGIYQTSNFR
VVPSPGDVVRFPNITNLCPFGEVFNATKFPSPVYAWERKKISNCVADYSVLY
NSTFFSTFKCYGVSATKLNLDLCSNVYADSFVVKGDDVRQIAPGQTGVIA
DYNKLPDDFMGCVLAWNTRNIDATSTGNVNYKYRYLRHGKLRPFERDI
SNVPFSPDGKPCTPPALNCYWPLNDYGFYTTTGIGYQPYRVVVLSEFLLNA
PATVCGPKLSTDLIKNQCVNFNENGLTGTGVLTPSSKRFQPFQFGRDVSD
FTDSVRDPKTSEILDSPCSFGGVS VITPGTNASSEVAVLYQDVNCTDVSTA
IHADQLTPAWRIYSTGNNVFQTQAGCLIGAEHVDTSYECDIPIGAGICASYH
TVSLLRSTSQKSIVAYTMSLGADSSIAYSNNTIAIPTNFSISITTEVMPV SMA
KTSVDCNMYICGDSTECANLLLQYGSFCTQLNRALSGIAAEQDRNTREVF
AQVKQMYKTPTLK YFGGFNFSQILPDPLKPTKRSFIEDLLFNKVT LADAGF
MKQYGECLGDINARDLICAQKFNGLTVLPPLLTDDMIAAYTAALVSGTAT
AGWTFGAGAALQIPFAMQMAYRFNGIGVTQNVLYENQKQIANQFNKAIS
QIQESLTTTSTALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRL
DKVEAEVQIDRLITGRLOSLQTYVTQQLIRAAEIRASANLAATKMSECVLG
QSKRVDFCGKGYHLMSFPQAAPHGVVFLHVTYVPSQERNFTTAPAICHEG
KAYFPREGVVFVNGTSWFITQRNFFSPQIITTDNTFVSGNCDVVIGIINNTVY
DPLQPELDSFKEELDKYFKNHTSPDVDLGDISGINASVVNIQKEIDRLNEVA
KNLNEIDLQELGKYEYIKWPWYVWLGFIAGLIAIVMVTILLCCMTSCC
SCLKGACSCGSCCKFDEDDSEPV LKGVKLHYT

**SEQ ID NO: 3 - Protein sequence for Spike protein amino acid 275-1081
from accession number AAP13441 (807aa) (wild type, wt):**

AVDCSQNPLAELKCSVKSFEIDKGIYQTSNFRVVPSPGDVVRFPNITNLC
PFGEVFNATKFPSVYAWERKKISNCVADYSVLYNSTFFSTFKCYGVSATK
LNDLCFSNVYADSFVVKGDDVRQIAPGQTGVIADYNYKLPDDFMGCVLA
WNTRNIDATSTGNYNKYRYLRHGKLRPFERDISNVPFSPDGKPCPPALN
CYWPLNDYGFYTTTGIGYQPYRVVVLSELLNAPATVCGPKLSTDLIKNO
CVNFFNFGLTGTGVLTPSSKRFQPFQQFGRDVSDFTDSVRDPKTSEILDISP
CSFGGVSIVTPGTNASSEVAVLYQDVNCTDVSTAIHADQLTPAWRIYSTGN
NVFQTQAGCLIGAEHVDTSYECDIPGAGICASYHTVSLLRSTSQKSIVAYT
MSLGADSSIAYSNNTIAIPTNFSISITTEVMPVSMAKTSVDCNMYICGDSTE
CANLLLQYGSFCTQLNRALSGIAAEQDRNTREVFAQVKQMYKTPTLKYFG
GFNFSQILPDPLKPTKRSFIEDLLFNKVTLADAGFMKQYGECLGDINARDLI
CAQKFNGLTVLPPLLTDDMIAAYTAALVSGTATAGWTFGAGAALQIPFAM
QMA YRFNGIGVTQNVLYENQKQLANQFNKAISQIQESLTTTSTALGKLQDV
VNQNAQALNTLVKQLSSNFGAISSVLNDILSRDKVEAEVQIDRLITGRLQS
LQTYVTQQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSFP
QAAPHGVVFLHVTYVPSQERNFTTAPAICHEGKAYFPREGVVFVNG

**SEQ ID NO: 4 - Protein sequence for Spike protein amino acid 275-1081
mutant with 9 potential N-linked glycosylation sites eliminated
(807aa)(substituted Alanine shown as "a")(mutant, mt):**

AVDCSQNPLAELKCSVKSFEDKGIYQTSNFRVVPSPGDVVRFPNlaNLCP
FGEVF_aATKFPSVYAWERKKISNCVADYSVL_{YN}S_aFFSTFKCYGVSATKLN
DLCFSNVYADSFVVKGDDVRQIAPGQTGVIADYNYKLPDDFMGCVLAWN
TRNIDATSTGNYNKYRYLRHGKLRPFERDISNVPFSPDGKPC_{TP}PALNCY
WPLNDYGFYTTTGIGYQP_{YR}VVLSFELLNAPATVCGPKLSTDLIKNQCV
NFNFNGLTGTGVLTPSSKRFQPFQQFGRDVSDF_{TD}SVRDPKTSEILDISPCS
FGGVSVITPGTNA_aSEVAVLYQDV_aCTDVSTAIHADQLTPAWRIYSTGNNV
FQTQAGCLIGA_{EH}VDTSYEC_{DI}PIGAGICASYHTVSLLRSTSQKSIVAYTMS
LGADSSIA_{YS}aNTIAIPTN_{Fa}ISITTEVMPVSM_{AK}TSVDCNMYICGDSTECAN
LLLQYGSFCTQLNRALSGIAAEQDRNTREVF_{AQ}VKQMYKTPTLKYFGGFN
{Fa}QILPDPLKPTKRSFIEDLLFNKVT{LAD}AGFMKQYGECLGDINARDLICAQ
KFNGLTVLPPLLTD_{DM}IAAYTAALVSGTATAGWTFGAGAALQIPFAMQM
AYRFNGIGVTQNVLYENQKQIANQFNKAISQIQESLTTTSTALGKLQDVVN
QNAQALNTLVKQLSSNFGA_{ISS}VLNDILSR_{LD}KVEAEVQIDRLITGRLQSLQ
TYVTQQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSPQA
APHGVVFLHVTYVPSQERN_{Fa}TAPAICHEGKAYFPREGVFVFNG

SEQ ID NO: 5 - The gene sequence for Spike protein amino acid 275-1081 mutant (807aa) with native virus codons and elimination of N-glycosylation sites (2421bp) (substituted nucleotides shown capitalized):

gctgttgattgttctcaaaatccacttgctgaactcaaatgctctgttaagagctttgagattgacaaaggaattacc
agacctctaatttcagggtgttcctcaggagatgttgtagattccctaattGcaaacttggtccttttgagaggtt
tttGCCgctactaaattcccttctgtctatgcatgggagagaaaaaatttctaattgtttgctgattactctgtgctcta
caactcaGcattttttcaacctttaagtgtatggcgtttctgccactaagttgaatgatctttgcttctcaatgtctatga
gattctttttagtcaaggagatgatgtaagacaaaatagcgccaggacaaaactgggttattgctgattataattataaat
tgccagatgattcatgggtgtgtccttgcttggaatactaggaacattgatgctacttcaactggtaattataattataaat
ataggtatcttagacatggcaagcttaggccctttgagagagacatatctaattgtgccttttccccctgatggcaaacctt
gcaccccactgctctaattgtattggccattaaatgattatggttttacaccactactggcattggctaccaaccttaca
gagttgtagtactttttgaacttttaaatgcacgggccacgggttggtgacaaaaattatccactgacctattaagaac
cagtggtgcaattttaatttaattggactcactgggtactgggtgtgtaactccttcttcaaagagatttcaaccatttcaacaat
ttggccgtgatgtttctgattcactgattccgttcgagatcctaaaacatctgaaatattagacattcacttgccttttgg
gggtgtaagtgaattacacctggaacaaatgctGcatctgaagttgctgttctatatcaagatgttGCctgactgatg
ttctacagcaattcatgcagatcaactcacaccagcttggcgcatatattctactggaaacaatgtattccagactcaag
caggctgtcttataggagctgagcatgtcgacacttcttatgagtgcgacattcctattggagctggcatttgtgctgta
ccatacagtttcttattacgtagtactagccaaaaatctattgtggcttatactatgtctttaggtgctgatagttcaattgctt
actctGCCaacaccattgctatacctactaactttGcaattagcattactacagaagtaatgcctgtttctatggctaaaa
cctccgtagattgtaatatgtacatctgcggagattctactgaatgtgctaatttgccttccaatatggtagcttttgcacac
aactaaatcgtgcactctcaggtattgctgctgaacaggatcgcaacacacgtgaagtgttcgctcaagtcaaaaaat
gtacaaaaccccaactttgaaatattttggtggttttaattttGcacaaatattacctgacctctaaagccaactaagagg
tcttttattgaggactgctctttaataagggtgacactcgctgatgctggcttcatgaagcaatatggcgaatgcctaggtg
atattaatgctagagatctcatttgtgcgcagaagttcaatggacttacagtgttgcacctctgctcactgatgatgatt
gctgcctacactgctgctctagtttagtggtactgccactgctggatggacatttgggtgctggcgtgctcttcaaatacctt
ttgctatgcaaatggcatataggttcaatggcattggagtaccacaaatgttctctatgagaacaaaaaacaatcgcca
accaatttaacaaggcgattagtc aaattcaagaatcacttacaacaacatcaactgcattgggcaagctgcaagacgtt
gttaaccagaatgctcaagcattaaacacacttgtaaacacttagctctaattttggtgcaatttcaagtgtgctaaatga
tatcctttcgcgacttgataaagtcgaggcggagggtacaaattgacagggttaattacaggcagacttcaaagccttcaaa
cctatgtaacacaacaactaatcagggtgctgaaatcagggttctgctaattctgctgctactaaatgtctgagtgtgt
tcttgacaatcaaaaagagttgacttttggaaagggtaccaccttatgtccttcccacaagcagccccgcattggtg
ttgtcttctacatgtcacgtatgtgccatcccaggagaggaaacttGccacagcgccagcaatttgcattgaaggcaa
agcactactccctcgtagagggtgttttgtgttaattggc

SEQ ID NO: 6 - The gene sequence for Spike protein amino acid 275-1081 mutant (807aa) with altered codon usage to enhance expression and elimination of N-glycosylation sites (2421bp):

GCCGTGGACTGCTCCCAGAACCCCTGGCCGAGCTGAAGTGCTCCGTGAAGT
CCTTCGAGATCGACAAGGGCATCTACCAGACCTCCAACCTCCGCGTGGTGCCCTC
CGGCGACGTGGTGCCTTCCCCAACATCGCCAACCTGTGCCCTTCGGCGAGGTG
TTCGCCGCCACCAAGTTCCTTCCGTGTACGCCTGGGAGCGCAAGAAGATCTCCA
ACTGCGTGGCCGACTACTCCGTGCTGTACAACTCCGCCTTCTTCTCCACCTTCAA
GTGCTACGGCGTGTCCGCCACCAAGCTGAACGACCTGTGCTTCTCCAACGTGTAC
GCCGACTCCTTCGTGGTGAAGGGCGACGACGTGCGCCAGATCGCCCCGGCCAGA
CCGGCGTGATCGCCGACTACAACTACAAGCTGCCCGACGACTTCATGGGCTGCGT
GCTGGCCTGGAACACCCGCAACATCGACGCCACCTCCACCGGCAACTACAATAC
AAGTACCGCTACCTGCGCCACGGCAAGCTGCGCCCTTCGAGCGCGACATCTCCA
ACGTGCCCTTCTCCCCGACGGCAAGCCCTGCACCCCCCGCCCTGAACTGCTA
CTGGCCCCCTGAACGACTACGGCTTCTACACCACCACCGGCATCGGCTACCAGCCC
TACCGCGTGGTGGTGTCTCCTTCGAGCTGCTGAACGCCCCCGCCACCGTGTGCG
GCCCCAAGCTGTCCACCGACCTGATCAAGAACCAGTGCGTGAACCTTCAACTTCAA
CGGCCTGACCGGCACCGGCGTGCTGACCCCTCCTCCAAGCGCTTCAGCCCTTC
CAGCAGTTCGGCCGCGACGTGTCCGACTTCACCGACTCCGTGCGCGACCCCAAGA
CCTCCGAGATCCTGGACATCTCCCCCTGCTCCTTCGGCGGCGTGTCCGTGATCAC
CCCCGGCACCAACGCCGCTCCGAGGTGGCCGTGCTGTACCAGGACGTGGCCTGC
ACCGACGTGTCCACCGCCATCCACGCCGACCAGCTGACCCCGCCTGGCGCATCT
ACTCCACCGGCAACAACGTGTTCCAGACCCAGGCCGGCTGCCTGATCGGCGCCGA
GCACGTGGACACCTCCTACGAGTGCGACATCCCCATCGGCGCCGGCATCTGCGCC
TCCTACCACACCGTGTCCCTGCTGCGCTCCACCTCCCAGAAGTCCATCGTGGCCT
ACACCATGTCCCTGGGCGCCGACTCCTCCATCGCCTACTCCGCCAACACCATCGC
CATCCCCACCAACTTCGCCATCTCCATCACCACCGAGGTGATGCCCGTGTCCATG
GCCAAGACCTCCGTGGACTGCAACATGTACATCTGCGGCGACTCCACCGAGTGCG
CCAACCTGCTGCTGCAGTACGGCTCCTTCTGCACCCAGCTGAACCGCGCCCTGTC
CGGCATCGCCGCCGAGCAGGACCGCAACACCCGCGAGGTGTTGCCCCAGGTGAAG
CAGATGTACAAGACCCCCACCCTGAAGTACTTCGGCGGCTTCAACTTCGCCCAGA
TCCTGCCCGACCCCTGAAGCCCACCAAGCGCTCCTTCATCGAGGACCTGCTGTT
CAACAAGGTGACCCTGGCCGACGCCGGCTTCATGAAGCAGTACGGCGAGTGCCCTG
GGCGACATCAACGCCCGCGACCTGATCTGCGCCCAAGAAGTTCAACGGCCTGACCG
TGCTGCCCCCCTGCTGACCGACGACATGATCGCCGCCTACACCGCCGCCCTGGT
GTCCGGCACCGCCACCGCCGGCTGGACCTTCGGCGCCGGCGCCCTGCAGATC
CCCTTCGCCATGCAGATGGCCTACCGCTTCAACGGCATCGGCGTGACCCAGAACG
TGCTGTACGAGAACCAGAAGCAGATCGCCAACCAAGTTCAACAAGGCCATCTCCCA
GATCCAGGAGTCCCTGACCACCACCTCCACCGCCCTGGGCAAGCTGCAGGACGTG
GTGAACCAGAACGCCAGGCCCTGAACACCCTGGTGAAGCAGCTGTCTTCAACT
TCGGCGCCATCTCCTCCGTGCTGAACGACATCCTGTCCCGCCTGGACAAGGTGGA
GGCCGAGGTGCAGATCGACCGCTGATCACCAGCCGCTGCAGTCCCTGCAGACC
TACGTGACCCAGCAGCTGATCCGCGCCGCCGAGATCCGCGCCTCCGCCAACCTGG
CCGCCACCAAGATGTCCGAGTGCGTGTGGGCCAGTCCAAGCGCGTGGACTTCTG
CGGCAAGGGCTACCACCTGATGTCTTCCCCAGGCCGCCCCCACGGCGTGGTG
TTCTTGCACGTGACCTACGTGCCCTCCAGGAGCGCAACTTCGCCACCGCCCCCG
CCATCTGCCACGAGGGCAAGGCCTACTTCCCCCGGAGGGCGTGTTCGTGTTCAA
CGGC

SEQ ID NO: 7 - Potential N-glycosylation sites within the protein sequence of the Spike protein amino acid 275-1081 (807aa) (wild type, wt) with potential N-glycosylation sites underlined.

AVDCSQNPLAELKCSVKSFIDKGIYQTSNFRVVPSPGDVVRFPNITNLC
 PFGEVFNATKFPSVYAWERKKISNCVADYSVLYNSTFFSTFKCYGVSATK
 LNDLCFSNVYADSFVVKGDDVRQIAPGQTGVIADYNYKLPDDFMGCVLA
 WNTRNIDATSTGNYNKYRYLRHGKLRPFERDISNVPFSPDGKPTPPALN
 CYWPLNDYGFYTTTGIGYQPYRVVVLSEFLLNAPATVCGPKLSTDLIKNQ
 CVNFNFNGLTGTGVLTPSSKRFQPFQQFGRDVSDFDTSVRDPKTSEILDISP
 CSFGGVSIVITPGTNAASSEVAVLYQDVNCTDVSTAIHADQLTPAWRIYSTGN
 NVFQTQAGCLIGAEHVDTSYECDIPIGAGICASYHTVSLRSTSQKSIVAYT
 MSLGADSSIAYSNNTIAIPTNFSISITTEVMPVSMAKTSVDCNMYICGDSTE
 CANLLQYGSFCTQLNRALSGIAAEQDRNTREVFAQVKQMYKTPTLKYFG
 GFNFSQILPDPLKPTKRSFIEDLLFNKVTLADAGFMKQYGECLGDINARDLI
 CAQKFNGLTVLPPLLTDDMIAAYTAALVSGTATAGWTFGAGAALQIPFAM
 QMAYRFNGIGVTQNVLYENQKQIANQFNKAISQIQESLTTTSTALGKLQDV
 VNQNAQALNTLVKQLSSNFGAISSVLNDILSRLDKVEAEVQIDRLITGRLQS
 LQTYVTQQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLSFP
 QAAPHGVVFLHVTYVPSQERNFTTAPAICHEGKAYFPREGVVFVNG

SEQ ID NO: 8 Amino acid sequence of Region II peptide

VLYNSAFFSTFKCYGVSATKLNDLCFSNVYADSFVVKGDDVRQIAPGQTGVIADY
 NYKLPDDFMGCVLAWNTRNIDATSTGNYNKYRYLRHGKLRPFERDISNVPFSP
 DGKPTPPALNCYWPLNDYGFYTTTGIGYQPYRVVVLSEFLLNAPATVCGPKLST
 DLIKNQCVNFNFNGLTGTGVLTPSSKRFQPFQQFGRDVSDFDTSVRDPKTSEILDIS
 PCSFGGVSIVITPGTNAASEVAVLYQDV

SEQ ID NO: 9 Amino acid sequence of Region III peptide

AEQDRNTREVFAQVKQMYKTPTLKYFGGFNFAQILPDPLKPTKRSFIEDLLFNKV
 TLADAGFMKQYGECLGDINARDLCAQKFNGLTVLPPLLTDDMIAAYTAALVSGT
 ATAGWTFGAGAALQIPFAMQMAYRFNGIGVTQNVLYENQKQIANQFNKAISQIQ
 ESLTTTSTALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRLDKVEAEV
 QIDRLITGRLQSLQTYVTQQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKG
 YHL

SEQ ID NO: 10 Amino acid sequence of Region IV peptide

VLYNSAFFSTFKCYGVSATKLNDLCFSNVYADSFVVKGDDVRQIAPGQTGVIADY
 NYKLPDDFMGCVLAWNTRNIDATSTGNYNKYRYLRHGKLRPFERDISNVPFSP
 DGKPTPPALNCYWPLNDYGFYTTTGIGYQPYRVVVLSEFLLNAPATVCGPKLST
 DLIKNQCVNFNFNGLTGTGVLTPSSKRFQPFQQFGRDVSDFDTSVRDPKTSEILDIS
 PCSFGGVSIVITPGTNAASEVAVLYQDVACTDVSTAIHADQLTPAWRIYSTGNNVF

QTQAGCLIGAEHVDTSYECDIPGAGICASYHTVSLRSTSQKSIVAYTMSLGADSS
IAYSANTIAIPTNFAISITTEVMPVSMKTSVDCNMYICGDSTECANLLLQYGSFCT
QLNRALSGIAAEQDRNTREVFAQVKQMYKTPTLKYFGGFNFAQILPDPLKPTKRS
FIEDLLFNKVTLADAGFMKQYGECLGDINARDLICAQKFNGLTVLPPLLTDDMIA
AYTAALVSGTATAGWTFGAGAALQIPFAMQMA YRFNGIGVTQNVLYENQKQIA
NQFNKAISQIQESLTTTSTALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDI
LSRLDKVEAEVQIDRLITGRLQSLQTYVTQQLIRAAEIRASANLAATKMSECVLGQ
SKRVDFCGKGYHL

SEQ ID NO: 11 Amino acid sequence of Region II peptide from Spike protein from accession number AAP13441(wild type)

VLNSTFFSTFKCYGVSATKLNDLCFSNVYADSFVVKGDDVRQIAPGQ
TGVIADYNYKLPDDFMGCVLAWNTRNIDATSTGNVNYKYRYLRHGKLRP
FERDISNVFPSPDGKPCTPPALNCYWPLNDYGFYTTTGIGYQPYRVVVLSE
ELLNAPATVCGPKLSTDLIKNQCVNFNFNGLTGTGVLTPSSKRFQPFQQFG
RDVSDFTDSVRDPKTSEILDISPCSFGGVSVITPGTNASSEVAVLYQDV

SEQ ID NO: 12 Amino acid sequence of Region III peptide from Spike protein from accession number AAP13441(wild type)

AEQDRNTREVFAQVKQMYKTPTLKYFGGFNFSQILPDPLKPTKRSFIED
LLFNKVTLADAGFMKQYGECLGDINARDLICAQKFNGLTVLPPLLTDDMI
AAYTAALVSGTATAGWTFGAGAALQIPFAMQMAYRFNGIGVTQNVLYEN
QKQIANQFNKAISQIQESLTTTSTALGKLQDVVNQNAQALNTLVKQLSSNF
GAISSVLNDILSRDKVEAEVQIDRLITGRLQSLQTYVTQQLIRAAEIRASAN
LAATKMSECVLGQSKRVDFCGKGYHL

SEQ ID NO: 13 Amino acid sequence of Region IV peptide from Spike protein from accession number AAP13441(wild type):

VLNSTFFSTFKCYGVSATKLNDLCFSNVYADSFVVKGDDVRQIAPGQTG
VIADYNYKLPDDFMGCVLAWNTRNIDATSTGNVNYKYRYLRHGKLRPFE
RDISNVFPSPDGKPCTPPALNCYWPLNDYGFYTTTGIGYQPYRVVVLSE
LNAPATVCGPKLSTDLIKNQCVNFNFNGLTGTGVLTPSSKRFQPFQQFGRD
VSDFTDSVRDPKTSEILDISPCSFGGVSVITPGTNASSEVAVLYQDVNCTDV
STAIHADQLTPAWRIYSTGNNVFQTQAGCLIGAEHVDTSECDIPIGAGICA
SYHTVSLLRSTSQKSIVAYTMSLGADSSIAYSNNTIAIPTNFSISITTEVMPVS
MAKTSVDCNMYICGDSTECANLLLQYGSFCTQLNRALSGIAAEQDRNTRE
VFAQVKQMYKTPTLKYFGGFNFSQILPDPLKPTKRSFIEDLLFNKVTLADA
GFMKQYGECLGDINARDLICAQKFNGLTVLPPLLTDDMIAAYTAALVSGT
ATAGWTFGAGAALQIPFAMQMAYRFNGIGVTQNVLYENQKQIANQFNKA
ISQIQESLTTTSTALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILS
RLDKVEAEVQIDRLITGRLQSLQTYVTQQLIRAAEIRASANLAATKMSECV
LGQSKRVDFCGKGYHL

SEQ ID NO: 14 Amino acid sequence of Region IV peptide from Spike protein from accession number AAP13441(wild type):

AVDCSQNPLAELKCSVKSFEDKGIYQTSNFRVVPBGDVVRFPNITNLCPFG
EVFNATKFPSVYAWERKKISNCVADYSVLYNSTFFSTFKCYGVSATKLN
LCFSNVYADSFVVKGDDVRQIAPGQTGVIADYNYKLPDDFMGCVLAWNT
RNIDATSTGNYNYKYRYLRHGKLRPFERDISNVPFSPDGKPCTPPALNCY
WPLNDYGFYTTTGIGYQPYRVVLSFELLNAPATVCGPKLSTDLIKNCV
NFNFNGLTGTGVLTPSSKRFQPFQQFGRDVSDFDTSVRDPKTSEILDSPCS
FGGVSVITPGTNASSEVAVLYQDVNCTDVSTAIHADQLTPAWRIYSTGNN
VFQTQAGCLIGAETHVDTSYECDIPIGAGICASYHTVSLRSTSQKSIVAYTM
SLGADSSIAYSNNTIAIPTNFSISITTEVMPVSMAKTSVDCNMYICGDSTEC
NLLLQYGSFCTQLNRALSGIAAEQDRNTREVFAQVKQMYKTPTLKYFGGF
NFSQILPDPLKPTKRSFIEDLLFNKVTADAGFMKQYGECLGDINARDLCA
QKFNGLTVLPPLLTDDMLAA YTAALVSGTATAGWTFGAGAALQIPFAMQ
MAYRFNGIGVTQNVLYENQKQIANQFNKAISQIQESLTTTSTALGKLQDVV
NQNAQALNTLVKQLSSNFGAISSVLNDILSRDKVEAEVQIDRLITGRLQSL
QTYVTQQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHL

SEQ ID NO: 15 Linker for nucleotide primer oligo #1

TCGCTCGAGAAAAGAGTGCTCTACAACTCAGCATT

SEQ ID NO: 16 Linker for nucleotide primer oligo #2

ATCTCTAGATTAAACATCTTGATATAGAACAGC

SEQ ID NO: 17 Linker for nucleotide primer oligo #3 TCGCTCGAG

AAAAGAGCTGAACAGGATCGCAACACA

SEQ ID NO: 18 Linker for nucleotide primer oligo #4

ATCTCTAGATTAAAGGTGGTAGCCCTTTCC

SEQ ID NO: 19 SARS Spike Glycoprotein Fragment synthetic DNA sequence with N-lined glycosylation site mutations (2421 bp)

GCCGTGGACTGCTCCCAGAACCCACTGGCCGAGCTGAAGTGCTCCGTGA
AGTCCTTCGAGATCGACAAGGGCATCTACCAGACCTCCAACCTCCGCGTG
GTGCCATCCGGCGACGTGGTGCGCTTCCCAAACATCGCCAACCTGTGCC

CATTCGGCGAGGTGTTTCGCCGCCACCAAGTTCCCATCCGTGTACGCCTG
GGAGCGCAAGAAGATCTCCAACCTGCGTGGCCGACTACTCCGTG
CTGTACAACTCCGCCTTCTTCTCCACCTTCAAGTGCTACGGCGTGTCCGC
CACCAAGCTGAACGACCTGTGCTTCTCCAACGTGTACGCCGACTCCTTCG
TGGTGAAGGGCGACGACGTGCGCCAGATCGCCCCAGGCCAGACCGGCGT
GATCGCCGACTACAACCTACAAGCTGCCAGACGACTTCATGGGCTGCGTG
CTGGCCTGGAACACCCGCAACATCGACGCCACCTCCACCGGCAACTACA
ACTACAAGTACCGCTACCTGCGCCACGGCAAGCTGCGCCCCATTCGAGCG
CGACATCTCCAACGTGCCATTCTCCCCAGACGGCAAGCCATGCACCCAC
CAGCCCTGAACTGCTACTGGCCACTGAACGACTACGGCTTCTACACCACC
ACCGGCATCGGCTACCAGCCATACCGCGTGGTGGTGTCTCCTTCGAGC
TGCTGAACGCCCCAGCCACCGTGTGCGGCCCAAAGCTGTCCACCGACCT
GATCAAGAACCAGTGCGTGAACCTTCAACTTCAACGGCCTGACCGGCACC
GGCGTGCTGACCCCATCCTCCAAGCGCTTCCAGCCATTCCAGCAGTTCGG
CCGCGACGTGTCCGACTTCACCGACTCCGTGCGCGACCCAAAGACCT
CCGAGATCCTGGACATCTCCCCATGCTCCTTCGGCGGGCGTGTCCGTGATC
ACCCAGGCACCAACGCCGCCTCCGAGGTGGCCGTGCTGTACCAGGACG
TGGCCTGCACCGACGTGTCCACCGCCATCCACGCCGACCAGCTGACCCC
AGCCTGGCGCATCTACTCCACCGGCAACAACGTGTTCCAGACCCAGGCC
GGCTGCCTGATCGGCGCCGAGCACGTGGACACCTCCTACGAGT
GCGACATCCCAATCGGCGCCGGCATCTGCGCCTCCTACCACACCGTGTC
CCTGCTGCGCTCCACCTCCAGAAGTCCATCGTGGCCTACACCATGTCCC
TGGGCGCCGACTCCTCCATCGCCTACTCCGCCAACACCATCGCCATCCCA
ACCAACTTCGCCATCTCCATCACCACCGAGGTGATGCCAGTGTCCATGGC
CAAGACCTCCGTGGACTGCAACATGTACATCTGCGGCGACTCCACCGAG
TGCGCCAACCTGCTGCTGCAGTACGGCTCCTTCTGCACCCAGCTGAACCG
CGCCCTGTCCGGCATCGCCGCCGAGCAGGACCGCAACACCCGCGAGGTG
TTCGCCCAAGGTGAAGCAGATGTACAAGACCCCAACCCTGAAGTACTTCG
GCGGCTTCAACTTCGCCCAGATCCTGCCAGACCCACTGAAGCCAACCAA
GCGCTCCTTCATCGAGGACCTGCTGTTCAACAAGGTGACCCTGGCCGAC
GCCGGCTTCATGAAGCAGTACGGCGAGTGCCTGGGCGACATCAACGCCC
GCGACCTGATCTGCGCCCAGAAGTTCAACGGCCTGACCGTGCTGCCACC
ACTGCTGACCGACGACATGATCGCCGCCTACACCGCCGCCCTGGTGTC
CGGCACCGCCACCGCCGGCTGGACCTTCGGCGCCGGCGCCGCCCTGCAG
ATCCCATTCGCCATGCAGATGGCCTACCGCTTCAACGGCATCGGCGTGAC
CCAGAACGTGCTGTACGAGAACCAGAAGCAGATCGCCAACCAGTTCAAC
AAGGCCATCTCCCAGATCCAGGAGTCCCTGACCACCACCTCCACCGCCCT
GGGCAAGCTGCAGGACGTGGTGAACCAGAACGCCCAAGGCCCT
GAACACCCTGGTGAAGCAGCTGTCCTCCAACCTTCGGCGCCATCTCCTCCG
TGCTGAACGACATCCTGTCCCGCCTGGACAAGGTGGAGGCCGAGGTGCA
GATCGACCGCCTGATCACCGGCCGCCTGCAGTCCCTGCAGACCTACGTG
ACCCAGCAGCTGATCCGCGCCGCCGAGATCCGCGCCTCCGCCAACCTGG
CCGCCACCAAGATGTCCGAGTGCGTGCTGGGCCAGTCCAAGCG
CGTGGACTTCTGCGGCAAGGGCTACCACCTGATGTCCTTCCCACAGGCC
GCCCCACACGGCGTGGTGTTCCTGCACGTGACCTACGTGCCATCCCAGG
AGCGCAACTTCGCCACCGCCCCAGCCATCTGCCACGAGGGCAAGGCCTA
CTTCCCACGCGAGGGCGTGTTTCGTGTTCAACGGC

SEQ ID NO: 20

SARs Spike glycoprotein Fragment I protein sequence without the N-linked glycosylation sites (807 amino acids encoded by SEQ ID NO: 19):

AVDCSQNPLAELKCSVKSFEDKGIYQTSNFRVPSGDVVRFPNIANLCPFGEVFAATKFPSVYA
WERKKISNCVADYSVLYNSAFFSTFKCYGVSATKLNDLCFSNVYADSFVVKGDDVRQIAPGQTGV
IADYNYKLPPDDFMGCVLAWNTRNIDATSTGNYNKYRYLRHGKLRPFERDISNVFPSPDGKPCPT
PALNCYWPLNDYGFTTTTGIGYQPYRVVLSFELLNAPATVCGPKLSTDLIKNCVNFNFNGLTG
TGVLTSSSRKFQPFQFGRDVSDFDTSVRDPKTSEILDSPCSFGGVSVITPGTNAASEVAVLYQ
DVACTDVSTAIHADQLTPAWRIYSTGNNVFQTQAGCLIGAEHVDTSYECDIPGAGICASYHTVSL
RSTSQKSIVAYTMSLGADSSIAYSANTIAIPTNFAISITTEVMPVSMAKTSVDCNMYICGDSTECANL
LLQYGSFCTQLNRALSGIAAEQDRNTREVFAQVKQMYKTPTLKYFGGFNFAQILPDLPKPTKRSFI
EDLLFNKVTLDAGFMKQYGECLGDINARDLICAQKFNGLTVLPPLLTDDMIAAYTAALVSGTATA
GWTFGAGAAALQIPFAMQMAYRFNGIGVTQNVLYENQKQIANQFNKAISQIQESLTTTSTALGKLQ
DVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDLKVEAEVQIDRLITGRLQSLQTYVTQQLIRAA
EIRASANLAATKMSCEVLGQSKRVDFCGKGYHLSFPQAAPHGVVFLHVTYVPSQERNFATAPAI
CHEGKAYFPREGVVFVNG

SEQ ID NO: 21: SARs Spike glycoprotein Fragment II synthetic DNA sequence with N-linked glycosylation site mutations (744bps):

GTGCTGTACAACCTCCGCCTTCTTCTCCACCTTCAAGTGCTACGGCGTGTC
CGCCACCAAGCTGAACGACCTGTGCTTCTCCAACGTGTACGCCGACTCCT
TCGTGGTGAAGGGCGACGACGTGCGCCAGATCGCCCCAGGCCAGACCGG
CGTGATCGCCGACTACAACCTACAAGCTGCCAGACGACTTCATGGGCTGC
GTGCTGGCCTGGAACACCCGCAACATCGACGCCACCTCCACCGGCAACT
ACAACCTACAAGTACCGCTACCTGCGCCACGGCAAGCTGCGCCCATTCGA
GCGCGACATCTCCAACGTGCCATTCTCCCCAGACGGCAAGCCATGCACC
CCACCAGCCCTGAACTGCTACTGGCCACTGAACGACTACGGCTTCTACAC
CACCACCGGCATCGGCTACCAGCCATAACCGCGTGGTGGTGTCTCCTTC
GAGCTGCTGAACGCCCCAGCCACCGTGTGCGGCCCAAAGCTGTCCACCG
ACCTGATCAAGAACCAGTGCGTGAACCTTCAACTTCAACGGCCTGACCGGC
ACCGGCGTGCTGACCCCATCTCCAAGCGCTTCCAGCCATTCCAGCAGTT
CGGCCGCGACGTGTCCGACTTCACCGACTCCGTGCGCGACCCAAAGACC
TCCGAGATCCTGGACATCTCCCCATGCTCCTTCGGCGGGCGTGTCGTGAT
CACCCAGGCACCAACGCCGCCTCCGAGGTGGCCGTGCTGTACCAGGAC
GTG

SEQ ID NO: 22: SARs Spike glycoprotein Fragment II protein sequence without the N-linked glycosylation sites (248 amino acids, encoded by SEQ ID 21):

VLYNSAFFSTFKCYGVSATKLNDLCFSNVYADSFVVKGDDVRQIAPGQTGVIADYNYKLPPDDFMG
CVLAWNTRNIDATSTGNYNKYRYLRHGKLRPFERDISNVFPSPDGKPCPTPALNCYWPLNDYG
FYTTTGIGYQPYRVVLSFELLNAPATVCGPKLSTDLIKNCVNFNFNGLTGTGVLTPSSSRKFQPF
QQFGRDVSDFDTSVRDPKTSEILDSPCSFGGVSVITPGTNAASEVAVLYQDV

SEQ ID NO: 23: SARS Spike glycoprotein Fragment III synthetic DNA sequence with N-linked glycosylation site mutations (834 bps):

GCCGAGCAGGACCGCAACACCCGCGAGGTGTTTCGCCCAGGTGAAGCAGA
TGTACAAGACCCCAACCCTGAAGTACTTCGGCGGCTTCAACTTCGCCCAG
ATCCTGCCAGACCCACTGAAGCCAACCAAGCGCTCCTTCATCGAGGACCT
GCTGTTCAACAAGGTGACCTTGGCCGACGCCGGCTTCATGAAGCAGTAC
GGCGAGTGCTTGGGCGACATCAACGCCCGCGACCTGATCTGCGCCAGA
AGTTCAACGGCCTGACCGTGCTGCCACCACTGCTGACCGACGACATGAT

CGCCGCCTACACCGCCGCCCTGGTGTCCGGCACCGCCACCGCCGGCTGG
ACCTTCGGGCGCCGGCGCCGCCCTGCAGATCCCATTTCGCCATGCAGATGG
CCTACCGCTTCAACGGCATCGGCGTGACCCAGAACGTGCTGTACGAGAA
CCAGAAGCAGATCGCCAACCAGTTCAACAAGGCCATCTCCCAGATCCAG
GAGTCCCTGACCACCACCTCCACCGCCCTGGGCAAGCTGCAGGACGTGG
TGAACCAGAACGCCCAGGCCCTGAACACCCTGGTGAAGCAGCTGTCCTC
CAACTTCGGGCGCCATCTCCTCCGTGCTGAACGACATCCTGTCCCGCCTGG
ACAAGGTGGAGGCCGAGGTGCAGATCGACCGCCTGATCACCGGCCGCCCT
GCAGTCCCTGCAGACCTACGTGACCCAGCAGCTGATCCGCGCCGCCGAG
ATCCGCGCCTCCGCCAACCTGGCCGCCACCAAGATGTCCGAGTGCCTGC
TGGGCCAGTCCAAGCGCGTGGACTTCTGCGGCAAGGGCTACCACCTG

SEQ ID NO: 24: SARs Spike glycoprotein Fragment III protein sequence without the N-linked glycosylation sites (278 amino acids, encoded by SEQ ID NO: 23):

AEQDRNTREVFAQVKQMYKTPTLKYFGGFNFAQILPDPLKPTKRSFIEDLLFNKVTADAGFMKQ
YGECLGDINARDLICAQKFNGTLVLPPLTDDMIAAYTAALVSGTATAGWTFGAGAALQIPFAMQ
MAYRFNGIGVTQNVLYENQKQIANQFNKAISQIQESLTTTSTALGKLQDVVNQNAQALNTLVKQLS
SNFGAISSVLNDILSRDLKVEAEVQIDRLITGRLQSLQTYVTQQLIRAAEIRASANLAATKMSECVLG
QSKRVDFCGKGYHL

SEQ ID NO: 25: SARs Spike glycoprotein Fragment IV synthetic DNA sequence with N-linked glycosylation site mutations (2034 bps):

GTGCTGTAACTCCGCCTTCTTCTCCACCTTCAAGTGCTACGGCGTGTCGCCACCAAGCT
GAACGACCTGTGCTTCTCCAACGTGTACGCCGACTCCTTCGTGGTGAAGGGCGACGACGTG
CGCCAGATCGCCCCAGGCCAGACCGGCGTGATCGCCGACTACAACTACAAGCTGCCAGAC
GACTTCATGGGCTGCGTGCTGGCCTGGAACACCCGCAACATCGACGCCACCTCCACCGGCA
ACTACAACCTACAAGTACCGCTACCTGCGCCACGGCAAGCTGCGCCATTTCGAGCGCGACAT
CTCCAACGTGCCATTCTCCCCAGACGGCAAGCCATGCACCCACAGCCCTGAACTGCTAC
TGGCCACTGAACGACTACGGCTTCTACACCACCACCGGCATCGGCTACCAGCCAAAGCTGTC
TGGTGGTGCTGTCTTCGAGCTGCTGAACGCCCCAGCCACCGTGTCGCGGCCAAAGCTGTC
CACCGACCTGATCAAGAACCAGTGCGTGAACCTTCAACTTCAACGGCCTGACCGGCACCGGC
GTGCTGACCCCATCTCCAAGCGCTTCCAGCCATTCCAGCAGTTTCGGCCGCGACGTGTCCG
ACTTCACCGACTCCGTGCGCGACCCAAAGACCTCCGAGATCCTGGACATCTCCCCATGCTC
CTTCGGCGGCGTGTCGGTGATCACCCAGGCACCAACGCCGCCCTCCGAGGTGGCCGTGCT
GTACCAGGACGTGGCCTGCACCGACGTGTCCACCGCCATCCACGCCGACCAAGCTGACCCC
AGCCTGGCGCATCTACTCCACCGGCAACAAGTGTTCAGACCCAGGCGCGGCTGCCTGATC
GGCGCCGAGCAGTGACACCTCTACGAGTGCACATCCCAATCGGCGCGCGCATCTGC
GCCTCTACCACACCGTGTCCTGCTGCGCTCCACCTCCAGAAAGTCCATCGTGGCTTACA
CCATGTCCCTGGGCGCCGACTCCTCCATCGCCTACTCCGCCAACACCATCGCCATCCCAAC
CAACTTCGCCATCTCCATCACACCGAGGTGATGCCAGTGTCATGGCCAAGACCTCCGTG
GACTGCAACATGTACATCTGCGGCGACTCCACCGAGTGCGCCAACCTGCTGCTGCAGTACG
GCTCCTTCTGCACCCAGCTGAACCGCGCCCTGTCCGGCATCGCCGCCGAGCAGGACCGCA
ACACCCGCGAGGTGTTCCGCCAGGTGAAGCAGATGTACAAGACCCCAACCCTGAAGTACTT
CGGCGGCTTCAACTTCGCCAGATCCTGCCAGACCCACTGAAGCCAACCAAGCGCTCCTTC
ATCGAGGACCTGCTGTTCAACAAGGTGACCCTGGCCGACGCGCGCTTCATGAAGCAGTACG
GCGAGTGCTGGGCGACATCAACGCCCGCGACCTGATCTGCGCCAGAAAGTTCAACGGCC
TGACCGTGCTGCCACCACTGCTGACCGACGACATGATCGCCGCCCTACACCGCGCCCTGGT
GTCCGGCACCGCCACCGCGCGCTGGACCTTCGGCGCGCGCGCGCCCTGCAGATCCCAT
CGCCATGCAGATGGCCTACCGCTTCAACGGCATCGGCGTGACCCAGAACGTGCTGTACGAG
AACCAGAAGCAGATCGCCAACCAGTTCAACAAGGCCATCTCCAGATCCAGGAGTCCCTGA
CCACCACCTCCACCGCCCTGGGCAAGCTGCAGGACGTGGTGAACCAGAACGCCAGGCC
TGAACACCCTGGTGAAGCAGCTGTCTCCAACCTTCGGCGCCATCTCCTCCGTGCTGAACGA
CATCCTGTCCCGCCTGGACAAGGTGGAGGCCGAGGTGCAGATCGACCGCCTGATCACCGG
CCGCTGCAGTCCCTGCAGACCTACGTGACCCAGCAGCTGATCCGCGCGCGCGAGATCCG
CGCCTCCGCCAACCTGGCCGCCAACAGATGTCCGAGTGCGTGCTGGGCCAGTCCAAGCG
CGTGGACTTCTGCGGCAAGGGCTACCACCTG

SEQ ID NO: 26: SARs Spike glycoprotein Fragment IV protein sequence without the N-linked glycosylation sites (678 amino acids, encoded by SEQ ID NO: 25):

VLYNSAFFSTFKCYGVSATKLNLCFSNVYADSFVVKGDDVRQIAPGQTGVIADYNYKLPDDFMG
CVLAWNTRNIDATSTGNVNYKYRYLRHGKLRPFERDISNVPFSPDGKPCTPPALNCYWPLNDYG
FYTTTGIGYQPYRVVLSFELLNAPATVCGPKLSTDLIKNQCVNFNFNGLTGTGVLTPSSKRFQPF
QQFGRDVSDFTDSVRDPKTSEILDSPCSFGGVSVITPGTNAASEVAVLYQDVACTDVSTAIHADQ
LTPAWRIYSTGNNVFQTQAGCLIGAEHVDTSYECDIPIGAGICASYHTVSLLRSTSQKSIVAYTMSL
GADSSIAYSANTIAIPTNFAISITTEVMPVSMAKTSVDCNMYICGDSTECANLLLQYGSFCTQLNRA
LSGIAAEQDRNTREVFAQVKQMYKTPTLKYFGGFNFAQILPDPLKPTKRSFIEDLLFNKVTADAG
FMKQYGECLGDINARDLCAQKFNGLTVLPPLTDDMIAAYTAALVSGTATAGWTFGAGAALQIPF
AMQMAYRFNGIGVTQNVLYENQKQIANQFNKAISQIQESLTTTSTALGKLQDVVNQNAQALNTLV
KQLSSNFGAISSVLNDILSRDKVEAEVQIDRLITGRLQSLQTYVTQQLIRAAEIRASANLAATKMSE
CVLGQSKRVDFCGKGYHL